

Amendments to the Specification:

Please replace the paragraph beginning at page 5, line 13, with the following amended paragraph:

--The invention provides ICOS polypeptides containing the extracellular Ig-like domain. Such polypeptides typically will contain the ligand binding domain, and thus may contain amino acid positions that are important for ligand binding. An ICOS polypeptide of the invention can be from a human or a non-human (e.g., non-human primate, mouse, or rat) source. As used herein, "polypeptide" means any chain of amino acids, regardless of length or post-translational modification (e.g., phosphorylation or glycosylation). An "ICOS polypeptide" is any polypeptide that is at least 5 amino acids in length (e.g., 5, 6, 7, 8, 9, 10, 25, 50, or more than 50 amino acids in length), and has an amino acid sequence that is the same as, or substantially homologous to, the corresponding portion of the wild-type ICOS protein having the amino acid sequence of SEQ ID NO:12. An ICOS polypeptide can have a length that corresponds to that of the full length, wild-type ICOS protein, or can be shorter than the full length, wild-type protein (e.g., can be a truncated ICOS protein or can contain deletions relative to the full-length protein.) "Homologous," as used herein in reference to polypeptides, refers to the amino acid sequence similarity between two polypeptides. When an amino acid position in both of the polypeptides is occupied by identical amino acids, then they are homologous at that position. Thus, by a "substantially homologous polypeptide" is meant a polypeptide containing an amino acid sequence that is largely, but not entirely, homologous to the amino acid sequence of a reference polypeptide. As defined herein, a substantially homologous ICOS polypeptide has an amino acid sequence that is at least 75% (e.g., 80%, 85%, 90%, 95%, or 99%) homologous to the corresponding portion of the wild type ICOS polypeptide with the amino acid sequence of SEQ ID NO:12. Sequences that are substantially homologous can be identified by comparing the sequences using standard software that is frequently available in sequence data banks (e.g., the BL2seq program available on the internet at the NCBI government website, [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov), or at the Fish and Richardson website, [www.fr.com](http://www.fr.com)).--